```
! Sequence: momp
! Sequence: incC
! Sequence: pomp91a
CLUSTAL W (1.83) multiple sequence alignment


momp            ------------------------------------------------------------
incC            ------------------------------------------------------------
pomp91a         MIQMRLWGFLFLSSFCQVSYLRANDVLLPLSGIHSGEDLELFTLRSSSPTKTTYSLRKDF


momp            ------------------------------MKKLLKSVLVFAALSSASSLQALPVG--
incC            ------------------------------------------------MTSPIPFQ--
pomp91a         IVCDFAGNSIHKPGAAFLNLKGDLFFINSTPLAALTFKNIHLGARGAGLFSESNVTFKGL


momp            ---------------NPAEPSLMIDGILWEGFGGDPCDPCATWCDAISMRVGYYGDFVF
incC            ---------------SSGDASFLAEQPQQLPSTSESQLVTQLLTMMKHTQALSETVLQQ
pomp91a         HSLVLENNESWGGVLTTSGDLSFINNTSVLCQNNISYGPGGALLLQGRKSKALFFRDNRG


momp            DRVLKTDVNKEFQMGAKPTTDTGNSAAPS----------------------------
incC            QRDRLPTASIILQVGGAPTGGAGAPFQPG----------------------------
pomp91a         TILFLKNKAVNQDESHPGYGGAVSSISPGSPITFADNQEILFQENEGELGGAIYNDQGAI


momp            ------------------------TLTARENPAYGRHMQDAEMFTNAACMALNIWDR--
incC            ------------------------PADDHHHPIPPPVVPAQIETEITTIRSELQLMR--
pomp91a         TFENNFQTTSFFSNKASFEELSIAATAISIHSGAIPYSLKTLLQKLGGAIHADYVHIRDC


momp            --FDVFCTLGATSGYLKGNSASFNLVGLFGDNENQKTVKAESVFNMSFDQSVVELYTDTT
incC            --STLQQSTKGARTGVLVVTAILMTISLLAIIIILAVLGFTG---VLFQVALLMQGETN
pomp91a         IGSIVFEENSATAGGAIAVNAVCDINAQGPVRFINNSALGLNGGAIYMQATGSILRLHAN


momp            ------------------------------------FAWSVGARAALWECGCATLG----
incC            ------------------------------------LIWAMVSGSIICFIALIG----
pomp91a         QGDIEFCGNKVRSQFHSHINSTSNFTNNAITIQGAPREFSLSANEGHRICFYDPIISATE


momp            ------------------------------------------------------------
incC            ------------------------------------------------------------
pomp91a         QYNSLYINHQRLLEAGGAVIFSGARLSPEHKKENKNKTSIINQPVRLCSGVLSIEGGAIL


momp            ------------------------------------ASFQYAQSKPKVEELNVLCNAAEF
incC            ------------------------------------TLGLILTNKNTPLPAS---------
pomp91a         AVRSFYQEGGLLALGPGSKLTTQGKNSEKDKIVITNLGFNLENLDSSDPAEIRATEKASI


momp            TINKPKGYVGKEFPLDLTAGTDAATG--------------------------------
incC            ------------------------------------------------------------
pomp91a         EISGVPRVYGHTESFYENHEYASKPYTTSIILSAKKLVTAPSRPEKDIQNLIIAESEYMG


momp            ---------------TKDASIDYHEWQASLALSYRLNMFTPYIGVKWSRASFDADTIRIA
incC            ------------------------------------------------------------
pomp91a         YGYQGSWEFSWSPNDTKEKKTIIASWTPTGEFSLDPKRRGSFIPTTLWSTFSGLNIASNI


momp            QPKSATAIFDTTTLNPTIAGAGDVKTGAEGQLGDTMQIVSLQLNKMKSRKSCGIAVGTTI
incC            ------------------------------------------------------------
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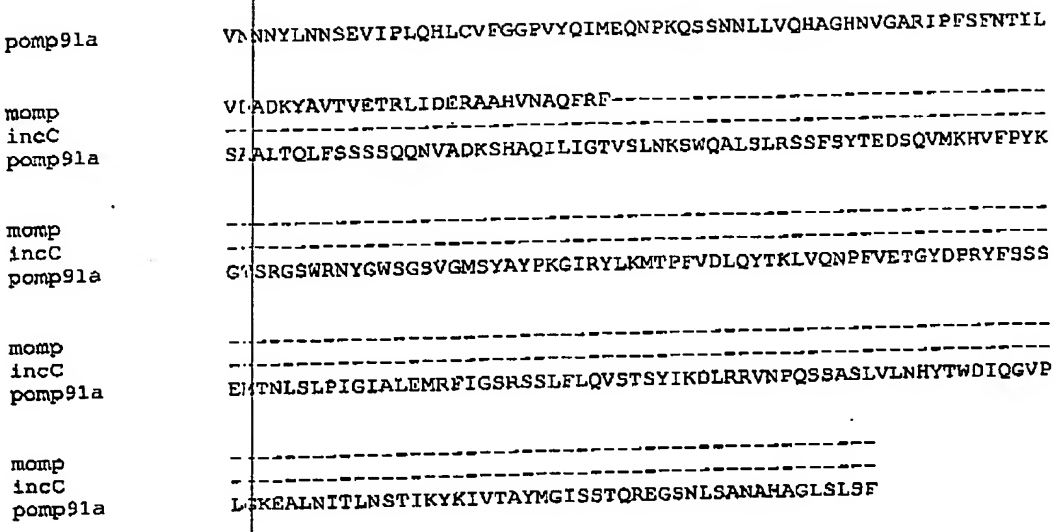

"*" means that the residues or nucleotides in that column are identical in all sequences in the alignment
":" means that conserved substitutions have been observed
"." means that semi-conserved substitutions are observed

6693087pomp91a seq
947 aa linear PAT 20-FEB-2004

LOCUS AAS37561
DEFINITION Sequence 3 from patent US 6693087.
ACCESSION AAS37561
VERSION AAS37561.1 GI:42715796
DBSOURCE accession AAS37561.1
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (residues 1 to 947)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding POMP91A protein of Chlamydia
JOURNAL Patent: US 6693087-A 3 17-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens: US 6693087
FEATURES Location/Qualifiers
source 1..947
/organism="unknown"

ORIGIN

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      1 mkqmrlwgfl flssfcqvsy lrandvllpl sgihsgedle lftlrssspt kttyslrkdf
     61 ivcdfagnsi nkpgaaflnl kgdlffinst plaaltfkni hlgargaglf sesnvtfkgl
    121 hslylennes wggvlttsgd lsfinntsvl cqnnisygpg galllqgrks kalffrdnrg
    181 tilflknkav nqdeshpgyg gavssispgs pitfadnqei lfqenegelg gaiyndqgai
    241 tfennfqtts ffsnkasfee lsiaataisi hsgaipyslk tllqklggai hadyvhirdc
    301 kgsivfeens ataggaiavn avcdinaqgp vrfinnsalg lnggaiymqa tgsilrlhan
    361 qgdiefcgnk vrsqfhshin stsnftnnai tiqgaprefs lsaneghric fydpiisate
    421 nynslyinhq rlleaggavi fsgarlspeh kkenknktsi inqpvrlcsg vlsieggail
    481 ayrsfyqegg llalgpgskl ttqgknsekd kivitnlgfn lenldssdpa eiratekasi
    541 eisgvprvyg htesfyenhe yaskpyttsi ilsakklvta psrpekdiqn liiaeseymg
    601 ygyqgswefs wspndtkekk tiiaswtptg efsldpkrrg sfipttlwst fsglniasni
    661 vnnnylnnse viplqhlcvf ggpvyqimeq npkqssnnll vqhaghnvga ripfsfntil
    721 saaltqlfss ssqqnvadks haqiligtvs lnkswqalsl rssfsyteds qvmkhvfpyk
    781 gtsrgswrny gwsgsvqmsy aypkgirylk mtpfvdlqyt klvqnpfvet gydpryfsss
    841 emtnlslpig lalemrfigs rsslflqvst syikdlrrvn pqssaslvln hytwdiqgvp
    901 lgkealnitl nstikykivt aymgisstqr egsnlsanah aglslsf
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6686339incc seq

LOCUS AAS33023 203 aa linear PAT 20-FEB-2004
DEFINITION Sequence 3 from patent US 6686339.
ACCESSION AAS33023
VERSION AAS33023.1 GI:42707452
DBSOURCE accession AAS33023.1
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (residues 1 to 203)
AUTHORS Murdin,A.D., Dunn,P.L. and Oomen,R.P.
TITLE Nucleic acid molecules encoding inclusion membrane protein C of Chlamydia
JOURNAL Patent: US 6686339-A 3 03-FEB-2004;
Aventis Pasteur Limited; Toronto;
CAX;
REMARK CAMBIA Patent Lens; US 6686339
FEATURES Location/Qualifiers
source 1..203
/organism="unknown"

ORIGIN
1 mtspipfqss qdasflaeqp qqlpstsesq lvtqlltmmk htqalsetvl qgqrdrlpta
61 siilqvggap tggagapfqp gpaddhhhpi pppvvpaqie teittirsel qlmrstlqqs
121 tkqartgvlv vtailmtisl laiiiiilav lgftgvlpqv allmqqetnl iwamvsgsii
181 cfialigtlg liltnkntpl pas

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                                        stephens momp
LOCUS       Q46409                        393 aa            linear   BCT 02-MAY-2006
DEFINITION  Major outer membrane protein, serovar D precursor (MOMP).
ACCESSION   Q46409
VERSION     Q46409  GI:6707730
DBSOURCE    swissprot: locus OM1D_CHLTR, accession Q46409;
            class: standard.
            created: May 30, 2000.
            sequence updated: Nov 1, 1996.
            annotation updated: May 2, 2006.
            xrefs: X62918.1, CAA44701.1, AF063195.2, AAC31436.2, AE001273.1,
            AAC68276.1, H71484
            xrefs (non-sequence databases): PHCI-2DPAGE:Q46409,
            GenomeReviews:AE001273_GR, InterPro:IPR000604, Pfam:PF01308,
            PRINTS:PR01334
KEYWORDS    Complete proteome; Ion transport; Membrane; Outer membrane; Porin;
            Signal; Transmembrane; Transport.
SOURCE      Chlamydia trachomatis
  ORGANISM  Chlamydia trachomatis
            Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
REFERENCE   1  (residues 1 to 393)
  AUTHORS   Sayada,C., Denamur,E. and Elion,J.
  TITLE     Complete sequence of the major outer membrane protein-encoding gene
            of Chlamydia trachomatis serovar Da
  JOURNAL   Gene 120 (1), 129-130 (1992)
  PUBMED    1398119
  REMARK    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
            STRAIN=D/B-120
REFERENCE   2  (residues 1 to 393)
  AUTHORS   Stothard,D.R., Boguslawski,G. and Jones,R.B.
  TITLE     Phylogenetic analysis of the Chlamydia trachomatis major outer
            membrane protein and examination of potential pathogenic
            determinants
  JOURNAL   Infect. Immun. 66 (8), 3618-3625 (1998)
  PUBMED    9673241
  REMARK    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
            STRAIN=D/IU-71960
REFERENCE   3  (residues 1 to 393)
  AUTHORS   Stephens,R.S., Kalman,S., Lammel,C., Fan,J., Marathe,R.,
            Aravind,L., Mitchell,W., Olinger,L., Tatusov,R.L., Zhao,Q.,
            Koonin,E.V. and Davis,R.W.
  TITLE     Genome sequence of an obligate intracellular pathogen of humans:
            Chlamydia trachomatis
  JOURNAL   Science 282 (5389), 754-759 (1998)
  PUBMED    9784136
  REMARK    NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
            STRAIN=D/UW-3/Cx
COMMENT     On Sep 27, 2005 this sequence version replaced gi:7442973.
            [FUNCTION] Structural rigidity of the outer membrane of elementary
            bodies and porin forming, permitting diffusion of solutes through
            the intracellular reticulate body membrane.
            [SUBUNIT] Disulfide bond interactions within and between MOMP
            molecules and other components form high molecular-weight
            oligomers.
            [SUBCELLULAR LOCATION] Bacterial cell outer membrane; multi-pass
            membrane protein.
            [SIMILARITY] Belongs to the chlamydial OMP family.
FEATURES             Location/Qualifiers
     source          1..393
                     /organism="Chlamydia trachomatis"
                     /db_xref="taxon:813"
     gene            1..393
                     /gene="ompA"
                     /locus_tag="CT_681"
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                                                stephens momp
                                /note="synonym: omp1"
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                                /gene="ompA"
                                /locus_tag="CT_681"
                                /product="Major outer membrane protein, serovar D
                                precursor"
     Region                     1..22
                                /gene="ompA"
                                /locus_tag="CT_681"
                                /region_name="Signal"
                                /inference="non-experimental evidence, no additional
                                details recorded"
                                /note="By similarity."
     Region                     23..393
                                /gene="ompA"
                                /locus_tag="CT_681"
                                /region_name="Mature chain"
                                /experiment="experimental evidence, no additional details
                                recorded"
                                /note="Major outer membrane protein, serovar D.
                                /FTId=PRO_0000020147."

ORIGIN
        1 mkklllksvlv faalssassl qalpvgnpae pslmidgilw egfggdpcdp catwcdaism
       61 rvgyygdfvf drvlktdvnk efqmgakptt dtgnsaapst ltarenpayg rhmqdaemft
      121 naacmalniw drfdvfctlg atsgylkgns asfnlvglfg dnenqktvka esvpnmsfdq
      181 svvelytdtt fawsvgaraa lwecgcatlg asfqyaqskp kveelnvlcn aaeftinkpk
      241 gyvgkefpld ltagtdaatg tkdasidyhe wqaslalsyr lnmftpyigv kwsrasfdad
      301 tiriaqpksa taifdtttln ptiagagdvk tgaegqlgdt mqivslqlnk mksrkscgia
      361 vgttivdadk yavtvetrli deraahvnaq frf
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